

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/542,682
Source: PCT
Date Processed by STIC: 07/28/2005

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PCT

RAW SEQUENCE LISTING

DATE: 07/28/2005

PATENT APPLICATION: US/10/542,682

TIME: 15:36:02

Input Set : A:\14875-147US1.txt

Output Set: N:\CRF4\07282005\J542682.raw

3 <110> APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA
 5 <120> TITLE OF INVENTION: Anti-PCI neutralizing antibodies
 7 <130> FILE REFERENCE: 14875-147US1
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/542,682
 C--> 9 <141> CURRENT FILING DATE: 2005-07-19
 9 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/000429
 10 <151> PRIOR FILING DATE: 2004-01-20
 12 <150> PRIOR APPLICATION NUMBER: JP 2003-011529
 13 <151> PRIOR FILING DATE: 2003-01-20
 15 <160> NUMBER OF SEQ ID NOS: 60
 17 <170> SOFTWARE: PatentIn version 3.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 27
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Artificial Sequence
 24 <220> FEATURE:
 25 <223> OTHER INFORMATION: Artificially synthesized sequence
 27 <400> SEQUENCE: 1
 28 acgaattcca ccatgcagct cttcctc 27
 30 <210> SEQ ID NO: 2
 31 <211> LENGTH: 28
 32 <212> TYPE: DNA
 33 <213> ORGANISM: Artificial Sequence
 35 <220> FEATURE:
 36 <223> OTHER INFORMATION: Artificially synthesized sequence
 38 <400> SEQUENCE: 2
 39 ctggatcctc aggggcgggt cactttgc 28
 41 <210> SEQ ID NO: 3
 42 <211> LENGTH: 26
 43 <212> TYPE: DNA
 44 <213> ORGANISM: Artificial Sequence
 46 <220> FEATURE:
 47 <223> OTHER INFORMATION: Artificially synthesized sequence
 49 <400> SEQUENCE: 3
 50 ttggatccgg ggttcacttt gccaaag 26
 52 <210> SEQ ID NO: 4
 53 <211> LENGTH: 1237
 54 <212> TYPE: DNA
 55 <213> ORGANISM: Artificial
 57 <220> FEATURE:
 58 <223> OTHER INFORMATION: Artificially synthesized sequence encoding human PCI
 60 <220> FEATURE:
 61 <221> NAME/KEY: CDS

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62 <222> LOCATION: (11)..(1228)

64 <400> SEQUENCE: 4

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65 gaattccacc atg cag ctc ttc ctc ctc ttg tgc ctg gtg ctt ctc agc 49
66      Met Gln Leu Phe Leu Leu Leu Cys Leu Val Leu Leu Ser
67      1          5          10
69 cct cag ggg gcc tcc ctt cac cgc cac cac ccc cgg gag atg aag aag 97
70 Pro Gln Gly Ala Ser Leu His Arg His His Pro Arg Glu Met Lys Lys
71      15          20          25
73 aga gtc gag gac ctc cat gta ggt gcc acg gtg gcc ccc agc agc aga 145
74 Arg Val Glu Asp Leu His Val Gly Ala Thr Val Ala Pro Ser Ser Arg
75      30          35          40          45
77 agg gac ttt acc ttc gac ctc tac agg gtc ttg gct tcc gct gcc ccc 193
78 Arg Asp Phe Thr Phe Asp Leu Tyr Arg Val Leu Ala Ser Ala Ala Pro
79      50          55          60
81 agc cag aat atc ttc ttc tcc cct gtg agc atc tcc atg agc ctg gcc 241
82 Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Ile Ser Met Ser Leu Ala
83      65          70          75
85 atg ctc tcc ctg ggg gct ggg tcc agc aca aag atg cag atc ctg gag 289
86 Met Leu Ser Leu Gly Ala Gly Ser Ser Thr Lys Met Gln Ile Leu Glu
87      80          85          90
89 ggc ctg ggc ctc aac ctc cag aaa agc tca gag gag gag ctg cac aga 337
90 Gly Leu Gly Leu Asn Leu Gln Lys Ser Ser Glu Glu Glu Leu His Arg
91      95          100          105
93 ggc ttt cag cag ctc ctt cag gaa ctc aac cag ccc aga gat ggc ttc 385
94 Gly Phe Gln Gln Leu Leu Gln Glu Leu Asn Gln Pro Arg Asp Gly Phe
95      110          115          120          125
97 cag ctg agc ctc ggc aat gcc ctt ttc acc gac ctg gtg gta gac ctg 433
98 Gln Leu Ser Leu Gly Asn Ala Leu Phe Thr Asp Leu Val Val Asp Leu
99      130          135          140
101 cag gac acc ttc gta agt gcc atg aag acg ctg tac ctg gca gac act 481
102 Gln Asp Thr Phe Val Ser Ala Met Lys Thr Leu Tyr Leu Ala Asp Thr
103      145          150          155
105 ttc ccc acc aac ttt agg gac tct gca ggg gcc atg aag cag atc aat 529
106 Phe Pro Thr Asn Phe Arg Asp Ser Ala Gly Ala Met Lys Gln Ile Asn
107      160          165          170
109 gat tat gtg gca aag caa acg aag ggc aag att gtg gac ttg ctt aag 577
110 Asp Tyr Val Ala Lys Gln Thr Lys Gly Lys Ile Val Asp Leu Leu Lys
111      175          180          185
113 aac ctc gat agc aat gcg gtc gtg atc atg gtg aat tac atc ttc ttt 625
114 Asn Leu Asp Ser Asn Ala Val Val Ile Met Val Asn Tyr Ile Phe Phe
115      190          195          200          205
117 aaa gct aag tgg gag aca agc ttc aac cac aaa ggc acc caa gag caa 673
118 Lys Ala Lys Trp Glu Thr Ser Phe Asn His Lys Gly Thr Gln Glu Gln
119      210          215          220
121 gac ttc tac gtg acc tcg gag act gtg gtg cgg gta ccc atg atg agc 721
122 Asp Phe Tyr Val Thr Ser Glu Thr Val Val Arg Val Pro Met Met Ser
123      225          230          235
125 cgc gag gat cag tat cac tac ctc ctg gac cgg aac ctc tcc tgc agg 769
126 Arg Glu Asp Gln Tyr His Tyr Leu Leu Asp Arg Asn Leu Ser Cys Arg

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127          240          245          250
129 gtg gtg ggg gtc ccc tac caa ggc aat gcc acg gct ttg ttc att ctc 817
130 Val Val Gly Val Pro Tyr Gln Gly Asn Ala Thr Ala Leu Phe Ile Leu
131          255          260          265
133 ccc agt gag gga aag atg cag cag gtg gag aat gga ctg agt gag aaa 865
134 Pro Ser Glu Gly Lys Met Gln Gln Val Glu Asn Gly Leu Ser Glu Lys
135 270          275          280          285
137 acg ctg agg aag tgg ctt aag atg ttc aaa aag agg cag ctc gag ctt 913
138 Thr Leu Arg Lys Trp Leu Lys Met Phe Lys Lys Arg Gln Leu Glu Leu
139          290          295          300
141 tac ctt ccc aaa ttc tcc att gag ggc tcc tat cag ctg gag aaa gtc 961
142 Tyr Leu Pro Lys Phe Ser Ile Glu Gly Ser Tyr Gln Leu Glu Lys Val
143          305          310          315
145 ctc ccc agt ctg ggg atc agt aac gtc ttc acc tcc cat gct gat ctg 1009
146 Leu Pro Ser Leu Gly Ile Ser Asn Val Phe Thr Ser His Ala Asp Leu
147          320          325          330
149 tcc ggc atc agc aac cac tca aat atc cag gtg tct gag atg gtg cac 1057
150 Ser Gly Ile Ser Asn His Ser Asn Ile Gln Val Ser Glu Met Val His
151          335          340          345
153 aaa gct gtg gtg gag gtg gac gag tgc gga acc aga gca gcg gca gcc 1105
154 Lys Ala Val Val Glu Val Asp Glu Ser Gly Thr Arg Ala Ala Ala Ala
155 350          355          360          365
157 acg ggg aca ata ttc act ttc agg tgc gcc cgc ctg aac tct cag agg 1153
158 Thr Gly Thr Ile Phe Thr Phe Arg Ser Ala Arg Leu Asn Ser Gln Arg
159          370          375          380
161 cta gtg ttc aac agg ccc ttt ctg atg ttc att gtg gat aac aac atc 1201
162 Leu Val Phe Asn Arg Pro Phe Leu Met Phe Ile Val Asp Asn Asn Ile
163          385          390          395
165 ctc ttc ctt ggc aaa gtg aac cgc ccc tgaggatcc 1237
166 Leu Phe Leu Gly Lys Val Asn Arg Pro
167          400          405
170 <210> SEQ ID NO: 5
171 <211> LENGTH: 406
172 <212> TYPE: PRT
173 <213> ORGANISM: Artificial
175 <220> FEATURE:
176 <223> OTHER INFORMATION: Human PCI
178 <220> FEATURE:
179 <221> NAME/KEY: sig_peptide
180 <222> LOCATION: (1)..(19)
182 <400> SEQUENCE: 5
183 Met Gln Leu Phe Leu Leu Leu Cys Leu Val Leu Leu Ser Pro Gln Gly
184 1          5          10          15
186 Ala Ser Leu His Arg His His Pro Arg Glu Met Lys Lys Arg Val Glu
187          20          25          30
189 Asp Leu His Val Gly Ala Thr Val Ala Pro Ser Ser Arg Arg Asp Phe
190          35          40          45
192 Thr Phe Asp Leu Tyr Arg Val Leu Ala Ser Ala Ala Pro Ser Gln Asn
193          50          55          60

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195 Ile Phe Phe Ser Pro Val Ser Ile Ser Met Ser Leu Ala Met Leu Ser
196 65 70 75 80
198 Leu Gly Ala Gly Ser Thr Lys Met Gln Ile Leu Glu Gly Leu Gly
199 85 90 95
201 Leu Asn Leu Gln Lys Ser Ser Glu Glu Glu Leu His Arg Gly Phe Gln
202 100 105 110
204 Gln Leu Leu Gln Glu Leu Asn Gln Pro Arg Asp Gly Phe Gln Leu Ser
205 115 120 125
207 Leu Gly Asn Ala Leu Phe Thr Asp Leu Val Val Asp Leu Gln Asp Thr
208 130 135 140
210 Phe Val Ser Ala Met Lys Thr Leu Tyr Leu Ala Asp Thr Phe Pro Thr
211 145 150 155 160
213 Asn Phe Arg Asp Ser Ala Gly Ala Met Lys Gln Ile Asn Asp Tyr Val
214 165 170 175
216 Ala Lys Gln Thr Lys Gly Lys Ile Val Asp Leu Leu Lys Asn Leu Asp
217 180 185 190
219 Ser Asn Ala Val Val Ile Met Val Asn Tyr Ile Phe Phe Lys Ala Lys
220 195 200 205
222 Trp Glu Thr Ser Phe Asn His Lys Gly Thr Gln Glu Gln Asp Phe Tyr
223 210 215 220
225 Val Thr Ser Glu Thr Val Val Arg Val Pro Met Met Ser Arg Glu Asp
226 225 230 235 240
228 Gln Tyr His Tyr Leu Leu Asp Arg Asn Leu Ser Cys Arg Val Val Gly
229 245 250 255
231 Val Pro Tyr Gln Gly Asn Ala Thr Ala Leu Phe Ile Leu Pro Ser Glu
232 260 265 270
234 Gly Lys Met Gln Gln Val Glu Asn Gly Leu Ser Glu Lys Thr Leu Arg
235 275 280 285
237 Lys Trp Leu Lys Met Phe Lys Lys Arg Gln Leu Glu Leu Tyr Leu Pro
238 290 295 300
240 Lys Phe Ser Ile Glu Gly Ser Tyr Gln Leu Glu Lys Val Leu Pro Ser
241 305 310 315 320
243 Leu Gly Ile Ser Asn Val Phe Thr Ser His Ala Asp Leu Ser Gly Ile
244 325 330 335
246 Ser Asn His Ser Asn Ile Gln Val Ser Glu Met Val His Lys Ala Val
247 340 345 350
249 Val Glu Val Asp Glu Ser Gly Thr Arg Ala Ala Ala Ala Thr Gly Thr
250 355 360 365
252 Ile Phe Thr Phe Arg Ser Ala Arg Leu Asn Ser Gln Arg Leu Val Phe
253 370 375 380
255 Asn Arg Pro Phe Leu Met Phe Ile Val Asp Asn Asn Ile Leu Phe Leu
256 385 390 395 400
258 Gly Lys Val Asn Arg Pro
259 405
262 <210> SEQ ID NO: 6
263 <211> LENGTH: 1261
264 <212> TYPE: DNA
265 <213> ORGANISM: Artificial
267 <220> FEATURE:

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268 <223> OTHER INFORMATION: Artificially synthesized DNA encoding human PCI with Flag-tag

270 <220> FEATURE:

271 <221> NAME/KEY: CDS

272 <222> LOCATION: (11)..(1258)

274 <400> SEQUENCE: 6

275 gaattccacc atg cag ctc ttc ctc ctc ttg tgc ctg gtg ctt ctc agc 49

276 Met Gln Leu Phe Leu Leu Leu Cys Leu Val Leu Leu Ser

277 1 5 10

279 cct cag ggg gcc tcc ctt cac cgc cac cac ccc cgg gag atg aag aag 97

280 Pro Gln Gly Ala Ser Leu His Arg His His Pro Arg Glu Met Lys Lys

281 15 20 25

283 aga gtc gag gac ctc cat gta ggt gcc acg gtg gcc ccc agc agc aga 145

284 Arg Val Glu Asp Leu His Val Gly Ala Thr Val Ala Pro Ser Ser Arg

285 30 35 40 45

287 agg gac ttt acc ttc gac ctc tac agg gtc ttg gct tcc gct gcc ccc 193

288 Arg Asp Phe Thr Phe Asp Leu Tyr Arg Val Leu Ala Ser Ala Ala Pro

289 50 55 60

291 agc cag aat atc ttc ttc tcc cct gtg agc atc tcc atg agc ctg gcc 241

292 Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Ile Ser Met Ser Leu Ala

293 65 70 75

295 atg ctc tcc ctg ggg gct ggg tcc agc aca aag atg cag atc ctg gag 289

296 Met Leu Ser Leu Gly Ala Gly Ser Ser Thr Lys Met Gln Ile Leu Glu

297 80 85 90

299 ggc ctg ggc ctc aac ctc cag aaa agc tca gag gag gag ctg cac aga 337

300 Gly Leu Gly Leu Asn Leu Gln Lys Ser Ser Glu Glu Glu Leu His Arg

301 95 100 105

303 ggc ttt cag cag ctc ctt cag gaa ctc aac cag ccc aga gat ggc ttc 385

304 Gly Phe Gln Gln Leu Leu Gln Glu Leu Asn Gln Pro Arg Asp Gly Phe

305 110 115 120 125

307 cag ctg agc ctc ggc aat gcc ctt ttc acc gac ctg gtg gta gac ctg 433

308 Gln Leu Ser Leu Gly Asn Ala Leu Phe Thr Asp Leu Val Val Asp Leu

309 130 135 140

311 cag gac acc ttc gta agt gcc atg aag acg ctg tac ctg gca gac act 481

312 Gln Asp Thr Phe Val Ser Ala Met Lys Thr Leu Tyr Leu Ala Asp Thr

313 145 150 155

315 ttc ccc acc aac ttt agg gac tct gca ggg gcc atg aag cag atc aat 529

316 Phe Pro Thr Asn Phe Arg Asp Ser Ala Gly Ala Met Lys Gln Ile Asn

317 160 165 170

319 gat tat gtg gca aag caa acg aag ggc aag att gtg gac ttg ctt aag 577

320 Asp Tyr Val Ala Lys Gln Thr Lys Gly Lys Ile Val Asp Leu Leu Lys

321 175 180 185

323 aac ctc gat agc aat gcg gtc gtg atc atg gtg aat tac atc ttc ttt 625

324 Asn Leu Asp Ser Asn Ala Val Val Ile Met Val Asn Tyr Ile Phe Phe

325 190 195 200 205

327 aaa gct aag tgg gag aca agc ttc aac cac aaa ggc acc caa gag caa 673

328 Lys Ala Lys Trp Glu Thr Ser Phe Asn His Lys Gly Thr Gln Glu Gln

329 210 215 220

331 gac ttc tac gtg acc tcg gag act gtg gtg cgg gta ccc atg atg agc 721

332 Asp Phe Tyr Val Thr Ser Glu Thr Val Val Arg Val Pro Met Met Ser

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/542,682

DATE: 07/28/2005
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Input Set : A:\14875-147US1.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:49; Xaa Pos. 2,3,4
Seq#:50; Xaa Pos. 4,5,6,7,9,10,14,17
Seq#:51; Xaa Pos. 6,7
Seq#:53; Xaa Pos. 10,13
Seq#:54; Xaa Pos. 1
Seq#:55; Xaa Pos. 3,6,7
Seq#:58; Xaa Pos. 8
Seq#:59; Xaa Pos. 2

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:4,5,6,7,57

VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49 after pos.:0
L:1254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50 after pos.:0
M:341 Repeated in SeqNo=50
L:1280 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51 after pos.:0
L:1316 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53 after pos.:0
L:1337 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54 after pos.:0
L:1365 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55 after pos.:0
L:1409 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:0
L:1427 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59 after pos.:0